

6

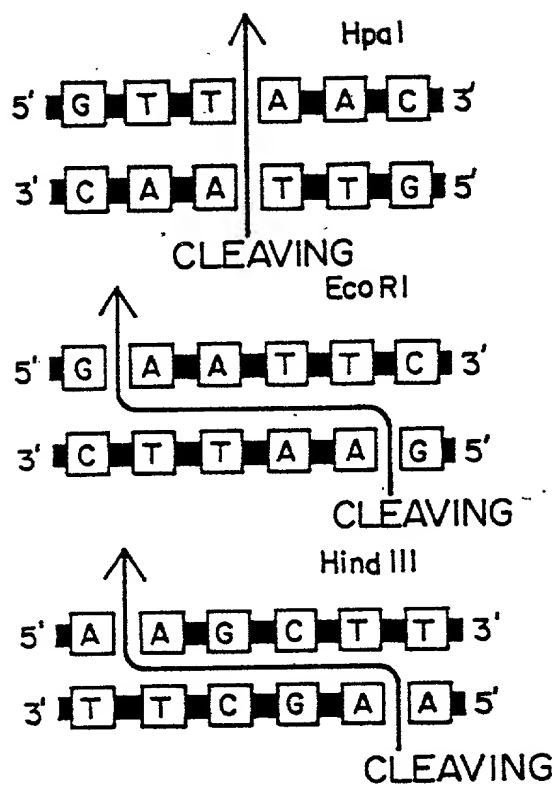


FIG. 1

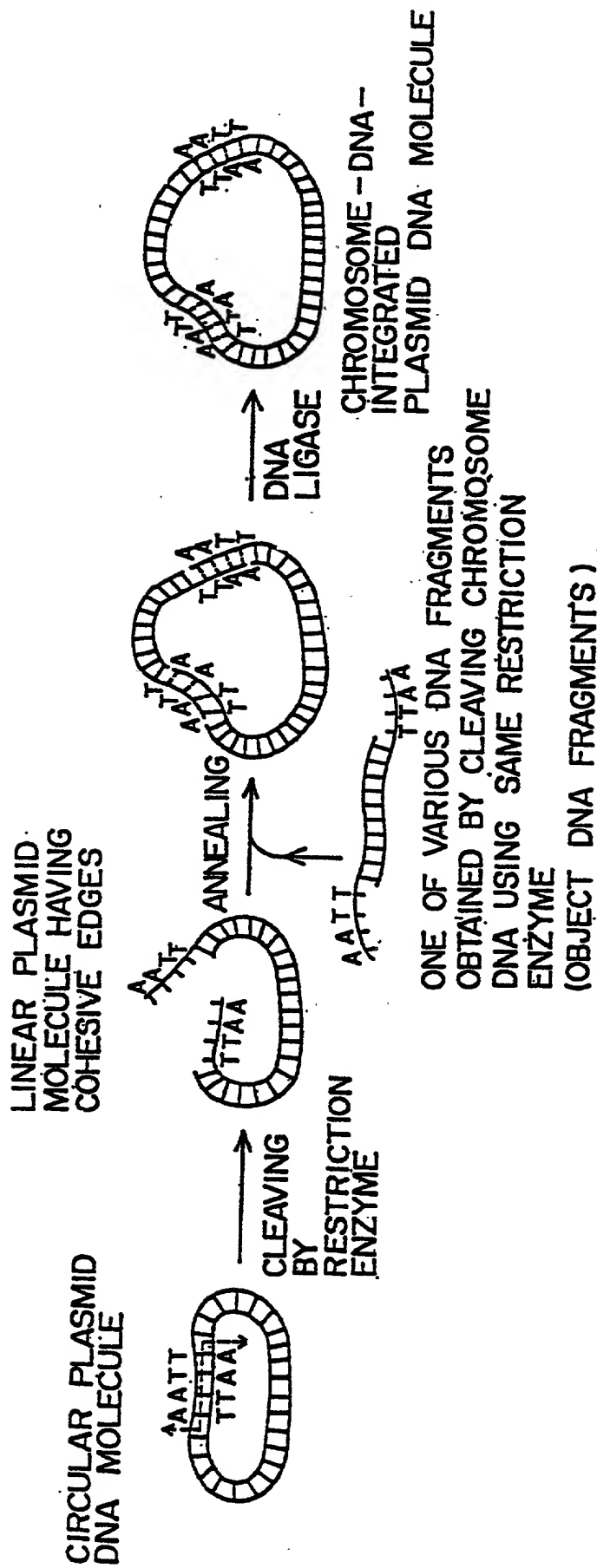


FIG. 2

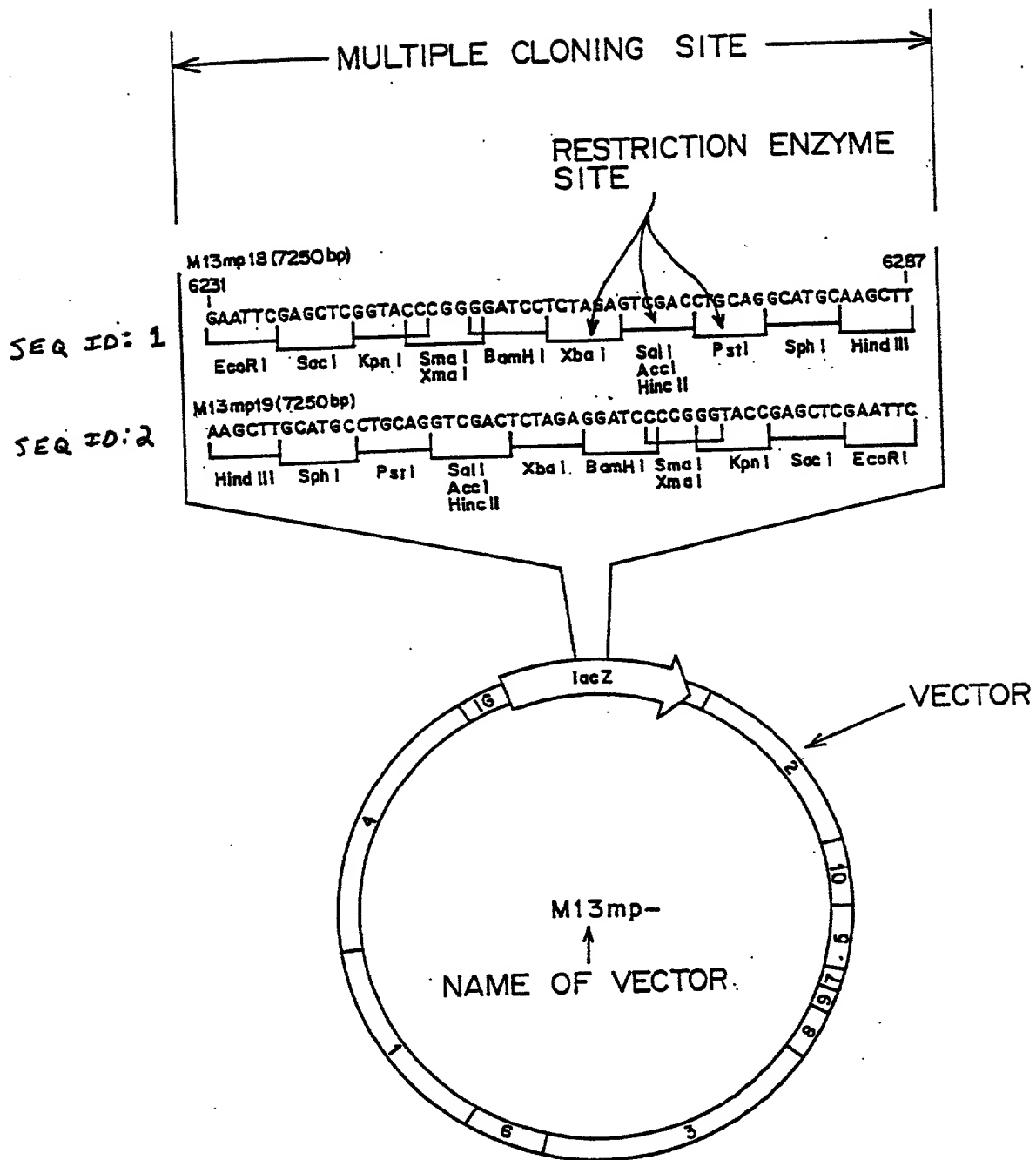
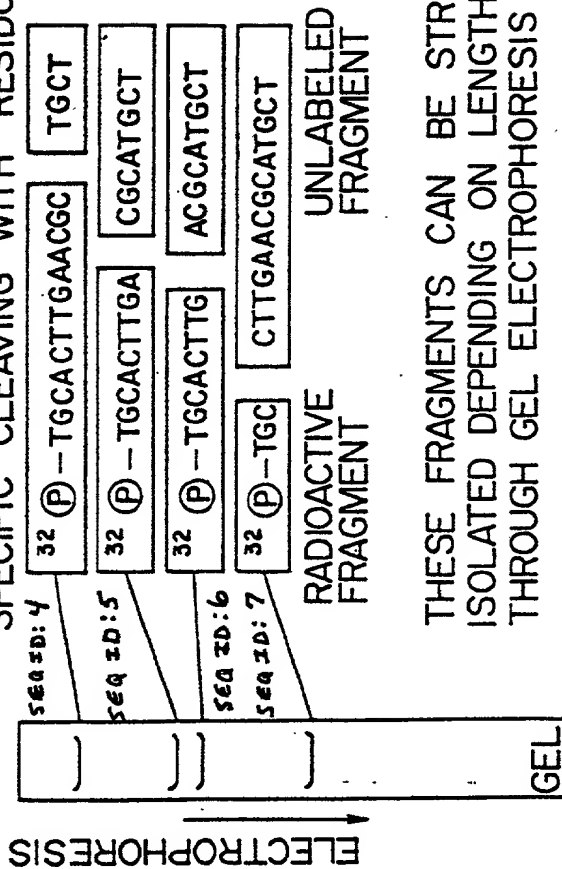


FIG. 3

DNA FRAGMENT LABELED WITH ^{32}P AT 5' EDGE

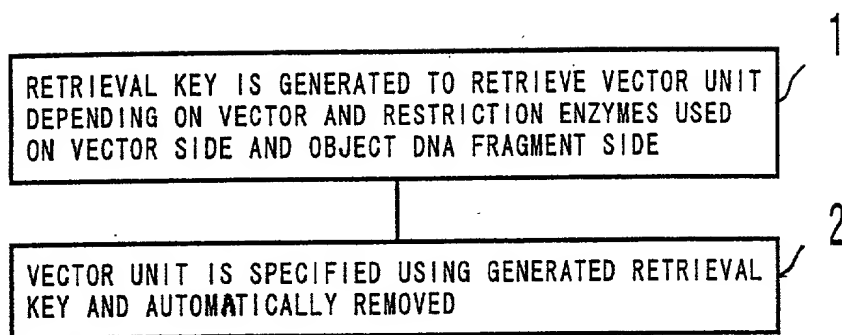
SEQ ID: 3 ^{32}P - TGCACCTTGAACGCATGCT

RADIOACTIVE FRAGMENTS OF VARIOUS LENGTHS THROUGH CHEMICAL PROCESS OF SPECIFIC CLEAVING WITH RESIDUAL BASE A



THESE FRAGMENTS CAN BE STRICTLY ISOLATED DEPENDING ON LENGTH THROUGH GEL ELECTROPHORESIS

FIG. 4



F I G . 5

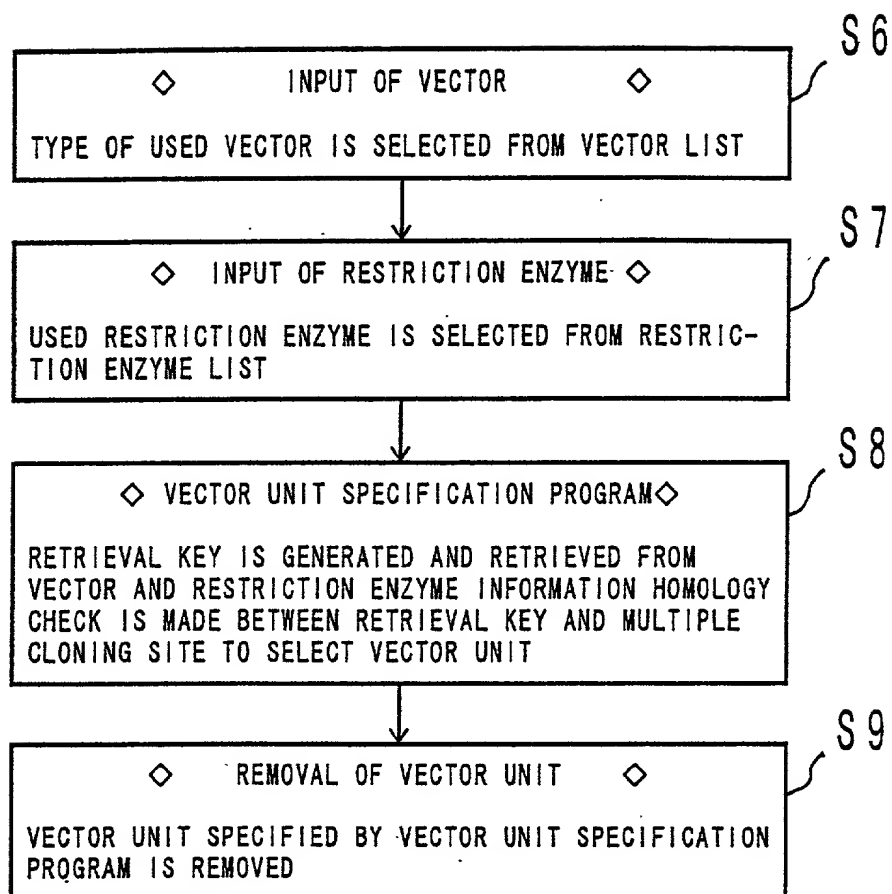


FIG. 6

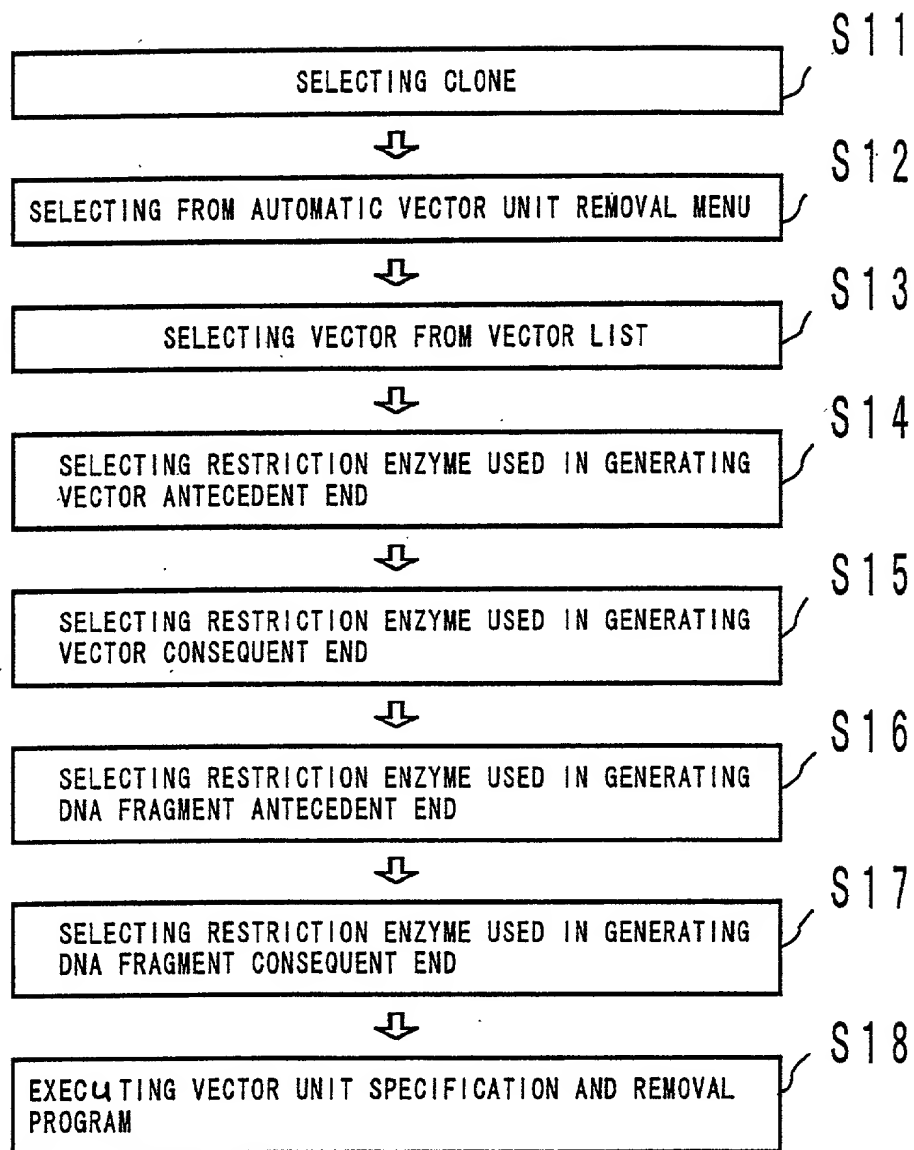


FIG. 7

09785269-052401
M1 3MP 1 8
M1 3MP 1 9
PBR 3 2 2
PSL 1 1 8 0
PSL 1 1 9 0
PT 7 T 3 1 8 U
PT 7 T 3 1 9 U
PTZ 1 8 R
PTZ 1 9 R
PUC 1 8
PUC 1 9, ETC.

FIG. 8

VECTOR DB FORMAT

```

>ID
PUC18
>SEQ 10: 8
TCGGCGGTTTCGGTGATGACGGTGAAAACCTCTGACACATGCAGCTCCCGGAGACGGTCACAGCTTGTCTGTAAGCGGAT
GCCGGGAGCAGACAAGCCCGTCAGGGCGCGTCAGCGGGTGTGGCGGGGTGTCGGGGCTGGCTTAACATATGCCGCATCAGA
GCAGATTGTACTGAGAGTGCACCATATGCGGTGTGAAATACCGCACAGATGCGTAAGGAGAAAAATACCGCATCAGGCGCC
ATTCCGCATTTCAGGCTGCGCAACTGTTGGGAAGGGCGATCGGTGCGGGCCTCTTCGCTATTACGCCAGCTGGCGAAAGGG
GGATGTGCTGCAAGGCGATTAAGTTGGGTAAACGCCAGGGTTTTCCAGTCACGACGTTGTAACGACGCGCCAGTGCCAA
GCTTGTCATGCTGCGAGTCTAGAGGATCCCGGGTACCGAGCTCGAATTGTAATCATGGTCATAGCTGTTTCTT
GTGTGAAATTGTTATCCGCTCACAATTCACACAACATACGAGCCGGAAGCATAAAGTGTAAAGCCTGGGGTGCCTAATG
AGTGAGCTAACTCACATTAATTGCGTTGCGCTCACTGCCCGCTTTCAGTCGGGAAACCTGTGTCGCGAGCTGCATTAAT
GAATCGGCCAACGCGCGGGGAGAGGCGGTTTTCGCTATTGGGCGCTCTTCCGCTTCTCGCTCACTGACTCGCTGCGCTCG
GTCGTTTCGGCTGCGGCGAGCGGTATCAGCTCAAAAGGCGGTAAACGCTTATCCACAGAATCAGGGGATAACGCAGG
AAAGAACATGTGAGCAAAAGGCCAGCAAAAGGCCAGGAACCGTAAAAAGGCCGCTTGTGGCGTTTTTCCATAGGCTCC
GCCCGCTGACGAGCATCACAAAAATCGACGCTCAAGTCAGAGGTGGCGAAACCGACAGGACTATAAGATACCGGCG
TTTTCCCGCTGGAAGCTCCCTCGTGGCTCTCCTGTTCCGACCCTGCCGCTTACCGGATACCTGTCCGCTTTTCTCCCTT
GGGAAGCGTGGCGTTTTCTCAAAGCTCAGCTGTAGGTATCTCAGTTTCGTTGAGGTGCTTTCGCTCCAAGCTGGGCTGTG
TGCAGAACCCCCCGTTTCAGCCCGACCGCTGCGCCTTATCCGGTAACTATCGTCTGAGTCAACCCGGTAAGACACGAC
TTATCGCCACTGGCAGCAGCCACTGGTAACAGGATTAGCAGAGCGAGGTATGTAGCGGCTGCTACAGAGTTCTTGAAGTG
GTGGCCTAACTACGGCTACACTAGAAGAACAGTATTTGGTATCTGCGCTCTGCTGAAGCCAGTTACCTTCGGAAGAG
TTGGTAGCTCTTGATCCGGCAAAACCAACCGCTGGTAGCGGTGGTTTTTTGTTTGAAGCAGCAGATTACGCGCAGA
AAAAAAGGATCTCAAGAAGATCCTTTGATCTTTTCTACGGGTCTGACGCTCAGTGGAACGAAAACTCACGTTAAGGGAT
TTTGGTCATGAGATTATCAAAAAGGATCTTCACCTAGATCCTTTTAAATTAATAATGAAGTTTTAAATCAATCTAAAGTA
TATATGAGTAAACTTGGTCTGACAGTTACCAATGCTTAATCAGTGAGGCACCTATCTCAGCGATCTGTCTATTTTCGTTCA
TCCATAGTTGCTGACTCCCCGTCGTGTAGATAACTACGATACGGGAGGGCTTACCATCTGGCCCCAGTGCTGCAATGAT
ACCGCGAGACCCACGCTCACC GGCTCCAGATTTATCAGCAATAAACCCAGCCAGCCGGAAGGGCCGAGCGCAGAAAGTGGTC
CTGCAACTTTATCCGCTCCATCCAGTCTATTAATTGTTGCCGGGAAGCTAGAGTAAGTAGTTTCGCCAGTTAATAGTTTG
CGCAACGTTGTTGCCATTGCTACAGGCATCGTGGTGTACGCTCGTTCGTTGTTGCTTTCATTTCAGCTCCGGTCCCA
ACGATCAAGGCGAGTTACATGATCCCCATGTTGTGCAAAAAAGCGGTTAGCTCCTTCGCTCCTCCGATCGTTGTGAGAA
GTAAGTTGGCCGAGTGTATCACTCATGGTTATGGCAGCACTGCATAATTCTTACTGTCATGCCATCCGTAAGATGC
TTTTCTGTGACTGTTGAGTACTCAACCAAGTCATTCTGAGAATAGTGTATGCGGCGACCGAGTTGCTCTTGGCCCGGCTC
AATACGGGATAATACCGCGGCACATAGCAGAACTTTAAAGTGCTCATCATTGGAAAACTTCTTCGGGGCGAAAACTCT
CAAGGATCTTACCGCTGTTGAGATCCAGTTCGATGTAACCCACTCGTGACCCCACTGATCTTCAGCATCTTTTACTTTC
ACCAGCGTTTCTGGGTGAGCAAAAACAGGAAGGCAAAATGCCGCAAAAAGGGAATAAGGGCGACACGGAAATGTTGAAT
ACTCATACTCTTCTTTTTCAATATTATTGAAGCATTATCAGGGTTATTGTCTCATGAGCGGATACATATTGTAATGTA
TTTAGAAAAATAACAAATAGGGGTTCCGCGCACATTTCCCGAAAAAGTGCCACCTGACGCTCTAAGAAACCATATTATC
ATGACATTAACCTATAAAAAATAGGCGTATCACGAGGCCCTTTCGTC
>MULTI
399..450

```

FIG. 9

(* INDICATES MULTIPLE CLONING SITE)

SEQ ID: 9 GTGCCAAGCTTGCATGCCCTGACGCTGACTCTAGAGGATCCCCGGGTACCGAGCTCGAATTCGTAAT

SEQ ID: 10 AAGCTT⇒HIND III

SEQ ID: 11 GCATGC⇒SPH I

SEQ ID: 12 CTGCAG⇒PST I

SEQ ID: 13 GTCGAC⇒SAL I, ACC I, HINC II

SEQ ID: 14 TCTAGA⇒XBA I

SEQ ID: 15 GGATCC⇒BAMH I

SEQ ID: 16 CCCGGG⇒SMA I, XMA I

SEQ ID: 17 GTACC⇒KPN I

SEQ ID: 18 GAGCTC⇒SAC I

SEQ ID: 19 GAATTC⇒ECOR I

FIG. 10

097855269 0524041
104250 159258/60

VECTOR SIDE

HIND III

SPH I

PST I

SAL I

ACC I

HINC II

XBA I

BAMH I

SMA I

XMA I

KPN I

SAC I

ECOR I

OBJECT DNA
FRAGMENT SIDE

HINDIII

SPH I

PST I

SAL I

ACC I

HINC II

XBA I

BAMH I

SMA I

XMA I

KPN I

SAC I

ECOR I

OTHER RESTRICTION
ENZYME

. . .

FIG. 11

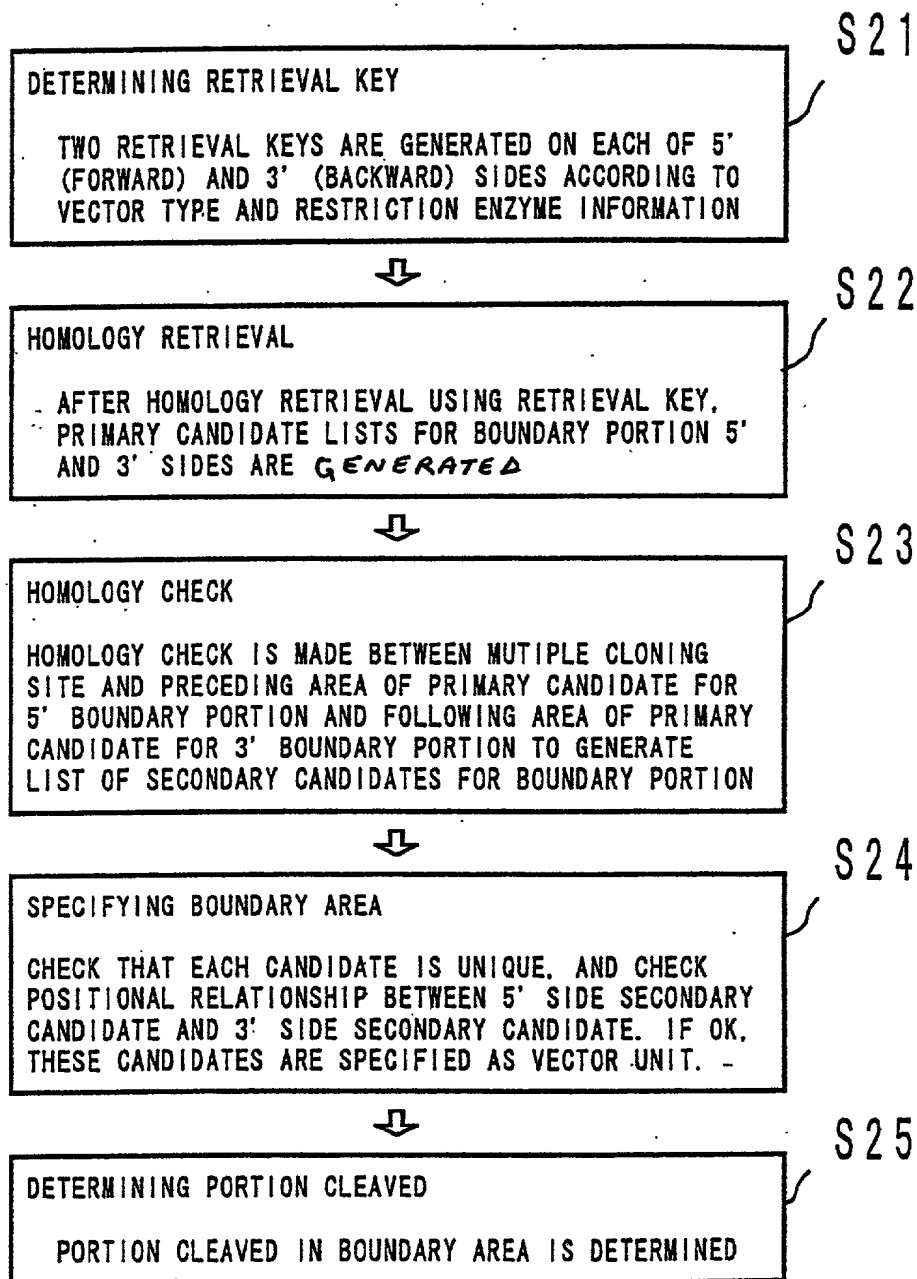


FIG. 12

WHEN SINGLE-STRANDED AREA IS FOUND ON 3' SIDE

STRAND A 5'	AREA A	AREA B3	AREA C	3'
	AREA C	AREA B3	AREA A	5'
← RESTRICTION ENZYME →				
SITE				

FIG. 13A

WHEN NO SINGLE-STRANDED AREA IS FOUND

STRAND A 5'	AREA A	AREA C	3'
	AREA C	AREA A	5'
← RESTRICTION ENZYME →			
SITE			

FIG. 13B

WHEN SINGLE-STRANDED AREA IS FOUND ON 5' SIDE

STRAND A 5'	AREA A	AREA B5	AREA C	3'
	AREA C	AREA B5	AREA A	5'
← RESTRICTION ENZYME →				
SITE				

FIG. 13C


```

graph TD
    S30[DOES SINGLE-STRANDED AREA IN RESTRICTION ENZYME SITE ON VECTOR 5' SIDE EXIST ? IF YES, WHICH SIDE IS IT LOCATED, 5' SIDE OR 3' SIDE ?]
    S31[DOES SINGLE-STRANDED AREA IN RESTRICTION ENZYME ON OBJECT DNA FRAGMENT 5' SIDE EXIST ON 5' SIDE ?]
    S32[IS [V1B5] EQUAL TO [F1B5] ?]
    S33[5' SIDE RETRIEVAL KEY IS DETERMINED TO BE [V1A] + [V1B5] + [F1C]]
    S34[MIS-SELECTION OF RESTRICTION ENZYME-GO TO RESTRICTION ENZYME SELECTING PROCESS.]
    S35[DOES SINGLE-STRANDED AREA OF RESTRICTION ENZYME EXIST IN RESTRICTION ENZYME SITE ON OBJECT DNA 5' SIDE ?]
    S36[5' SIDE RETRIEVAL KEY IS DETERMINED TO BE [V1A] + [F1C]]
    S37[DOES SINGLE-STRANDED AREA IN RESTRICTION ENZYME ON OBJECT DNA 5' SIDE EXIST ON 3' SIDE ?]
    S38[IS [V1B3] EQUAL TO [F1B3] ?]
    S39[5' SIDE RETRIEVAL KEY IS DETERMINED TO BE [V1A] + [V1B3] + [F1C]]

    S30 --> S31
    S30 --> S35
    S30 --> S37
    S31 -- Yes --> S32
    S31 -- No --> S35
    S32 -- Yes --> S33
    S32 -- No --> S35
    S35 -- Yes --> S36
    S35 -- No --> S37
    S37 -- Yes --> S38
    S37 -- No --> S35
    S38 -- Yes --> S39
    S38 -- No --> S36
    S36 --> S34
    S33 --> S34
    S39 --> S34

```

FIG. 15

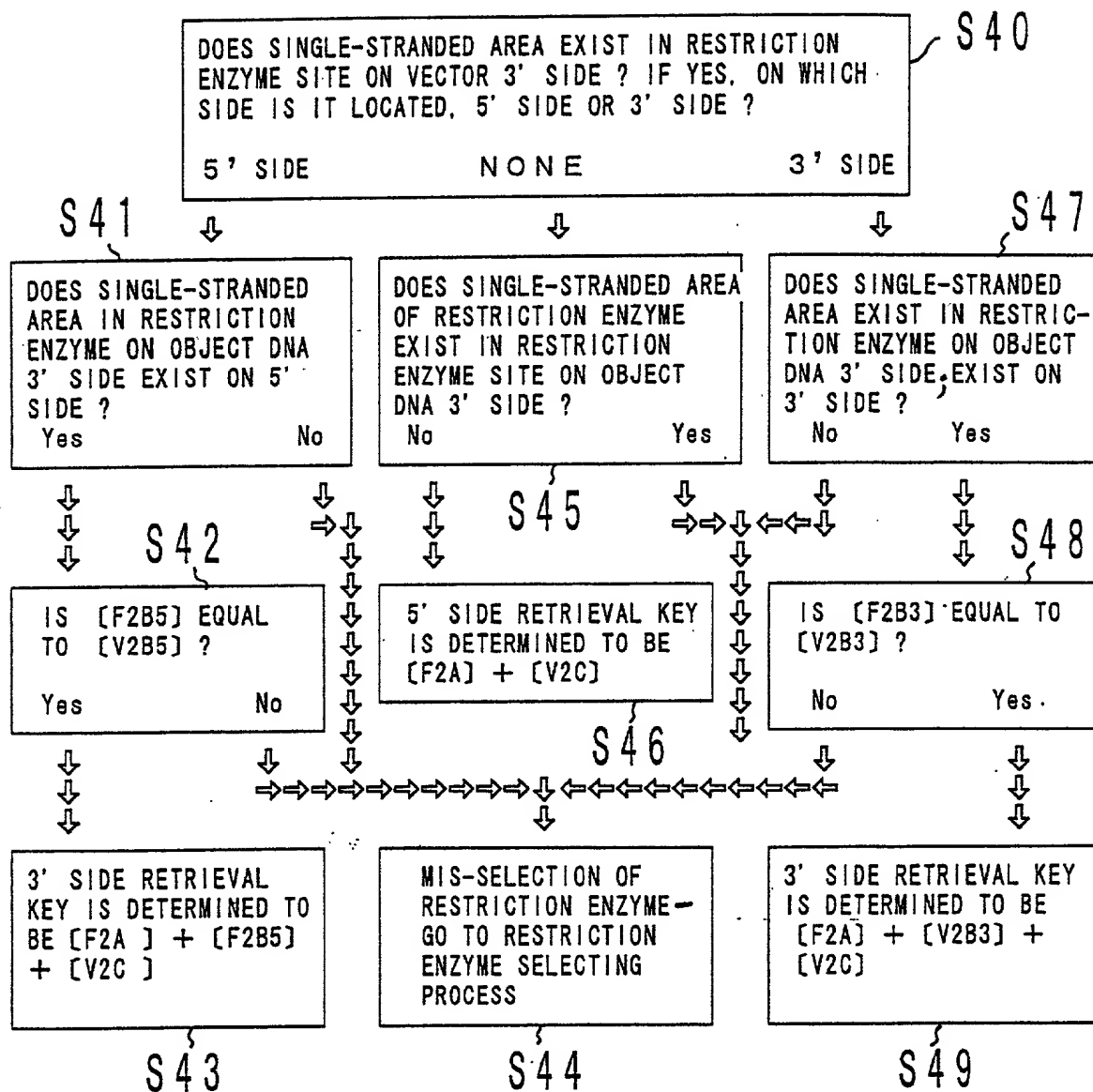


FIG. 16

A

(****) INDICATES RESIDUAL MULTIPLECLONING SITE
(+++++) INDICATES AN OBJECT DNA FRAGMENT

GTGCCAAGCTT+++++TCTAGAGGATCCCCGGGTACCGAGCTCGAATTCTGTAAT
AAGCTT TCTAGA
↑ ↑

5' SIDE RETRIEVAL KEY 9' SIDE RETRIEVAL KEY
(IN THIS EXAMPLE, (IN THIS EXAMPLE, XBA I SITE)
HIND III SITE)

FIG. 17

TOP SECRET 6929269

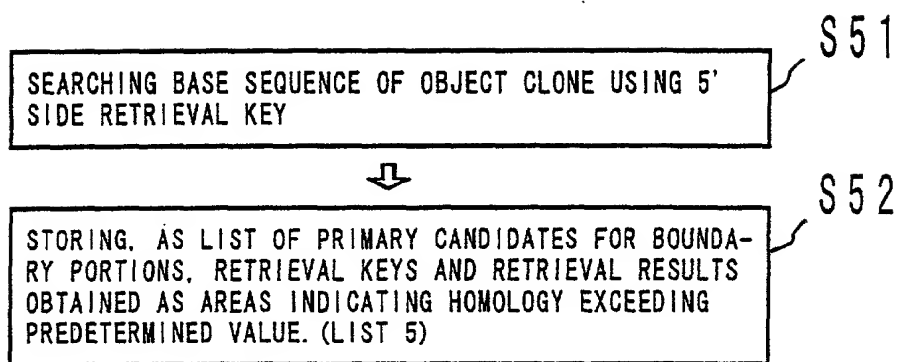


FIG. 18

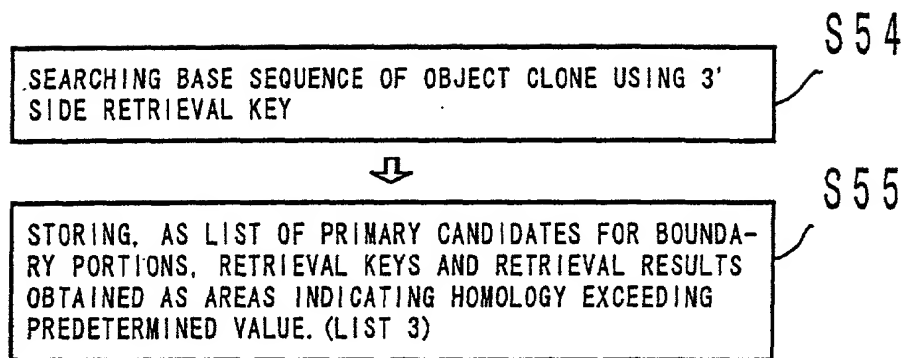


FIG. 19

DEFINING, IN MULTIPLE CLONING SITE OF VECTOR, RESTRICTION ENZYME SITE USED IN SHEARING 5' SIDE IN MULTIPLE CLONING SITE OF VECTOR AND AREA OUTSIDE ON 5' SIDE AS 5' SIDE RESIDUAL MULTIPLE CLONING SITE (5MCS)

S 6 1



WHEN VECTOR DB CONTAINS BASE SEQUENCE OTHER THAN MULTIPLE CLONING SITE, SUM OF 5MCS AND 5 BASES ON 5' SIDE FROM 5MCS IS DEFINED AS 5' SIDE RESIDUAL VECTOR AREA (5VA). IF VECTOR DB CONTAINS ONLY BASE SEQUENCE OF MULTIPLE CLONING SITE IN VECTOR DB, THEN 5 MCS IS 5VA.

S 6 2

(A HOMOLGY CHECK IS MADE ACCORDING TO FOLLOWING FLOWCHART ON ALL ELEMENTS IN PRIMARY CANDIDATES FOR BOUNDARY PORTIONS (LIST 5) OBTAINED IN 5' SIDE HOMOLGY RETRIEVAL)

DEFINING EACH CANDIDATE IN LIST 5 AND SEQUENCE AREA OUTSIDE ON 5' SIDE AS HOMOLGY CHECK AREA (5HCA) FOR CORRESPONDING CANDIDATE

S 6 3



COMPARING NUMBER OF BASES IN 5' SIDE RESIDUAL VECTOR AREA (5VA), NUMBER OF BASES OF 5HCA, AND NUMBER OF BASES 20, AND DEFINING SMALLEST NUMBER OF BASES AS NUMBER OF BASES FOR USE IN HOMOLGY CHECK (HCB)

S 6 4



EXTRACTING HCB BASES FROM 3' SIDE OF 5VA TO CHECK HOMOLGY TO HCB BASES ON 3' SIDE OF 5HCA

S 6 5



WHEN CONSTANT HOMOLGY IS OBTAINED, EXTRACTED BASES ARE DEFINED AS SECONDARY CANDIDATES FOR 5' SIDE BOUNDARY PORTIONS.

S 6 6

F I G . 2 0

09785569 052401

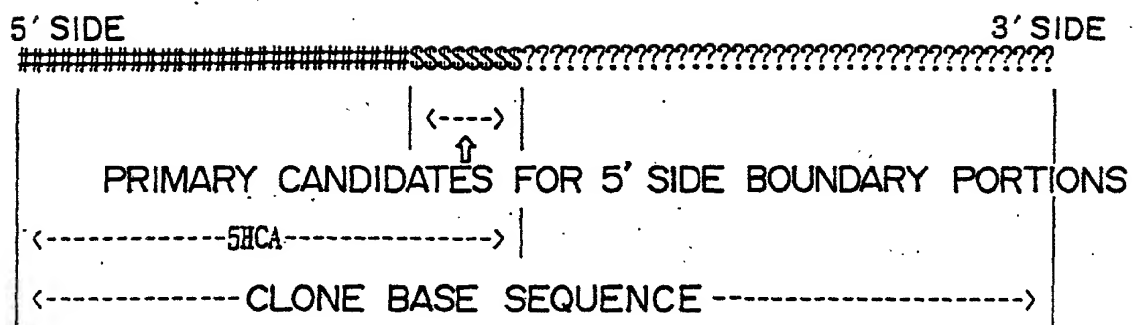


FIG. 21

DEFINING, IN MULTIPLE CLONING SITE OF VECTOR, RESTRICTION ENZYME SITE USED IN SHEARING 3' SIDE IN MULTIPLE CLONING SITE OF VECTOR AND AREA OUTSIDE ON 3' SIDE AS 3' SIDE RESIDUAL MULTIPLE CLONING SITE (3MCS)

S71



WHEN VECTOR DB CONTAINS BASE SEQUENCE OTHER THAN MULTIPLE CLONING SITE, SUM OF 3MCS AND 5 BASES ON 3' SIDE FROM 3MCS IS DEFINED AS 3' SIDE RESIDUAL VECTOR AREA (3VA). IF VECTOR DB CONTAINS ONLY BASE SEQUENCE OF MULTIPLE CLONING SITE IN VECTOR DB, THEN 3MCS IS 3VA.

S72

(A HOMOLGY CHECK IS MADE ACCORDING TO FOLLOWING FLOWCHART ON ALL ELEMENTS OF PRIMARY CANDIDATES FOR BOUNDARY PORTIONS (LIST 3) OBTAINED IN 3' SIDE HOMOLGY RETRIEVAL)

DEFINING EACH CANDIDATE IN LIST 3 AND SEQUENCE AREA OUTSIDE ON 3' SIDE AS HOMOLGY CHECK AREA (3HCA) FOR CORRESPONDING CANDIDATE

S73



COMPARING NUMBER OF BASES IN 3' SIDE RESIDUAL VECTOR AREA (3VA), NUMBER OF BASES OF 3HCA, AND NUMBER OF BASES 20, AND DEFINING SMALLEST NUMBER OF BASES AS NUMBER OF BASES FOR USE IN HOMOLGY CHECK (HCB)

S74



EXTRACTING HCB BASES FROM 5' SIDE OF 3VA TO CHECK HOMOLGY TO HCB BASES ON 5' SIDE OF 3HCA

S75



WHEN CONSTANT HOMOLGY IS OBTAINED, EXTRACTED BASES ARE DEFINED AS SECONDARY CANDIDATES FOR 3' SIDE BOUNDARY PORTIONS.

S76

F I G . 2 2

0978569-05401
104250-69258460

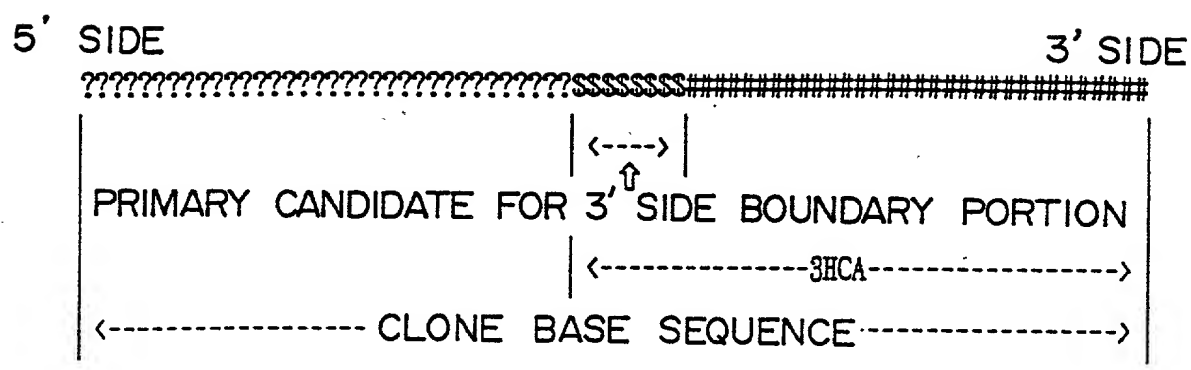


FIG. 23

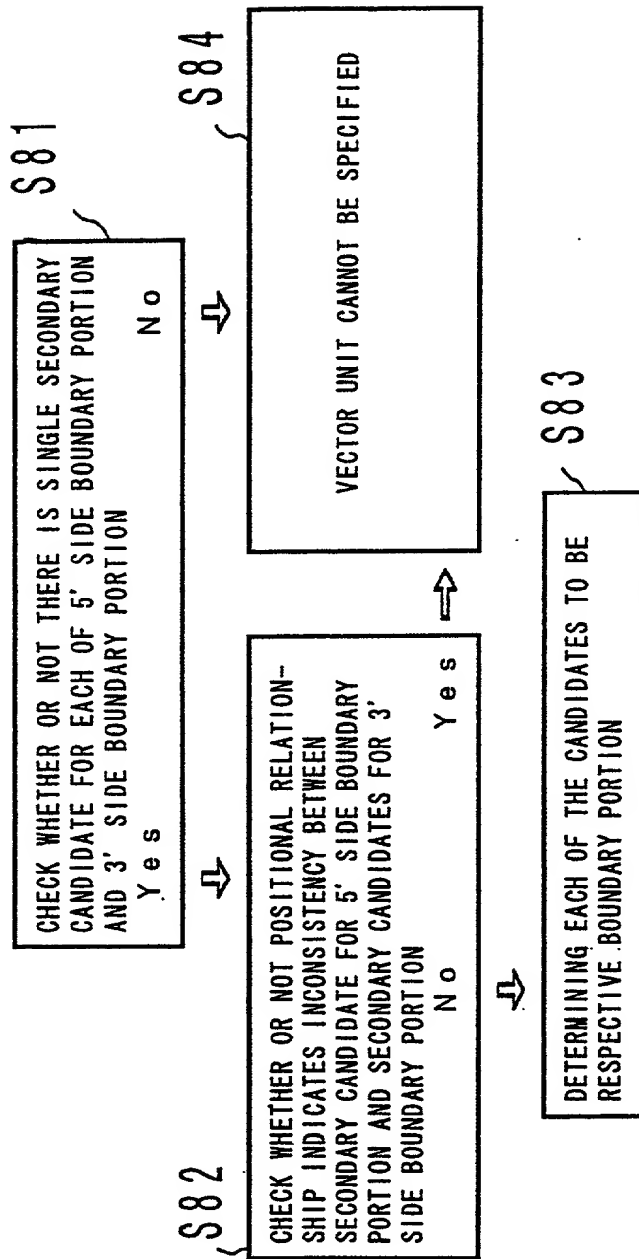


FIG. 24